SEQUENCE LISTING

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<110>  Istituto Superiore di Sanità
       National Institutes of Health

<120>  COLORECTAL ANTIGEN

<130>  WPP88367

<150>  US 60/512,040
<151>  2003-10-15

<160>  20

<170>  PatentIn version 3.3

<210>  1
<211>  1413
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (85)..(1395)

<220>
<221>  misc_feature
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<223>  nucleotide sequence encoding the immunogenic peptide

<400>  1
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cctgcatccc atgactcgga gctg atg gcc ttc atg acg agg aag ttg tgg         111
                          Met Ala Phe Met Thr Arg Lys Leu Trp
                          1               5

gac ctg gag cag cag gtg aag gcc cag act gat gag ata ctg tcc aag        159
Asp Leu Glu Gln Gln Val Lys Ala Gln Thr Asp Glu Ile Leu Ser Lys
10              15              20              25

gat cag aag ata gcg gcc cta gag gac ctg gtg cag acc ctc cgg cca        207
Asp Gln Lys Ile Ala Ala Leu Glu Asp Leu Val Gln Thr Leu Arg Pro
            30              35              40

cac cca gcc gag gca acc ctg cag cgg cag gag gaa ctg gag acg atg        255
His Pro Ala Glu Ala Thr Leu Gln Arg Gln Glu Glu Leu Glu Thr Met
            45              50              55

tgt gtg cag ctg cag cgg cag gtc agg gag atg gag cgg ttc ctc agt        303
Cys Val Gln Leu Gln Arg Gln Val Arg Glu Met Glu Arg Phe Leu Ser
            60              65              70

gac tat ggc ctg cag tgg gtg ggc gag ccc atg gac cag gag gac tca        351
Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp Gln Glu Asp Ser
        75              80              85

gag agc aag aca gtc tca gag cat ggc gag agg gac tgg atg aca gcc        399
Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp Trp Met Thr Ala
90              95              100             105

aag aag ttc tgg aag cca ggg gac tca ttg gcg ccc cct gag gtg gac        447
Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro Pro Glu Val Asp
                110             115             120

ttt gac agg ctg ctg gcc agc ctg cag gat ctt agt gag ctg gtg gta        495
Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser Glu Leu Val Val
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                125                    130                    135

gag ggt gac acc caa gtg aca cca gtg ccc ggc ggg gca cgg ctg cgt        543
Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly Ala Arg Leu Arg
        140                    145                    150

acc ctc gag ccc atc ccg ctg aag ctc tac cgg aat ggc atc atg atg        591
Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn Gly Ile Met Met
    155                    160                    165

ttc gac ggg ccc ttc cag ccc ttc tac gat ccc tcc aca cag cgc tgc        639
Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser Thr Gln Arg Cys
170                    175                    180                    185

ctc cga gac ata ttg gat ggc ttc ttt ccc tca gag ctc cag cga ctg        687
Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu Leu Gln Arg Leu
                190                    195                    200

tac ccc aat ggg gtc ccc ttt aag gtg agt gac ttg cgc aat cag gtc        735
Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu Arg Asn Gln Val
                205                    210                    215

tac ctg gag gat gga ctg gac ccc ttc cca ggc gag ggc cgt gtg gtg        783
Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu Gly Arg Val Val
        220                    225                    230

ggc agg cag cgg atg cac aag gcc ttg gac agg gtg gag gag cac cca        831
Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val Glu Glu His Pro
    235                    240                    245

ggc tcc agg atg act gct gag aaa ttt ctg aac agg ctc ccc aag ttt        879
Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg Leu Pro Lys Phe
250                    255                    260                    265

gtg atc cgg caa ggc gag gtg att gac atc cgg ggc ccc atc agg gac        927
Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly Pro Ile Arg Asp
                270                    275                    280

acc ttg cag aac tgc tgc cca ttg cct gcc cgg atc cag gag att gtg        975
Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile Gln Glu Ile Val
                285                    290                    295

gtg gag acg ccc acc ttg gcc gct gag cga gag agg agc cag gag tca        1023
Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg Ser Gln Glu Ser
        300                    305                    310

ccc aac aca ccg gca ccc ccg ctc tcc atg ctg cgc atc aag tct gag        1071
Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg Ile Lys Ser Glu
    315                    320                    325

aat ggg gaa cag gcc ttc cta ctg atg atg cag cct gac aac acc att        1119
Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro Asp Asn Thr Ile
330                    335                    340                    345

ggg gac gtg cga gct ctg cta gcg cag gcc agg gtc atg gat gcc tct        1167
Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp Ala Ser
                350                    355                    360

gcc ttt gag atc ttc agc aca ttc ccg ccc acc ctc tac cag gac gat        1215
Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp
                365                    370                    375

aca ctc acg ctg cag gct gca ggc ctt gtg ccc aaa gca gca ctg ctg        1263
Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala Leu Leu
        380                    385                    390

ctg cgg gca cgc cga gcc ccg aag tcc agc ctg aaa ttc agt cct ggt        1311
Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys Phe Ser Pro Gly
```

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     395                    400    .              405
ccc tgt ccc ggt ccc ggt ccc ggc ccc agt ccc ggt ccc ggt ccc ggc        1359
Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly Pro Gly Pro Gly
410                  415.             420                  425

tcc agt ccc tgt ccc gga ccc agt. ccc agc ccc caa taaagcaccc            1405
Ser Ser Pro Cys Pro Gly Pro Ser Pro Ser Pro Gln
                430              435

acccccctc                                                              1413
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<210>  2
<211>  437
<212>  PRT
<213>  Homo sapiens

<400>  2

Met Ala Phe Met Thr Arg Lys Leu Trp Asp Leu Glu Gln Gln Val Lys
1               5               10                  15


Ala Gln Thr Asp Glu Ile Leu Ser Lys Asp Gln Lys Ile Ala Ala Leu
            20              25                  30


Glu Asp Leu Val Gln Thr Leu Arg Pro His Pro Ala Glu Ala Thr Leu
        35              40                  45


Gln Arg Gln Glu Glu Leu Glu Thr Met Cys Val Gln Leu Gln Arg Gln
    50                  55                  60


Val Arg Glu Met Glu Arg Phe Leu Ser Asp Tyr Gly Leu Gln Trp Val
65                  70              75                  80


Gly Glu Pro Met Asp Gln Glu Asp Ser Glu Ser Lys Thr Val Ser Glu
                85                  90                  95


His Gly Glu Arg Asp Trp Met Thr Ala Lys Lys Phe Trp Lys Pro Gly
            100.                105                 110


Asp Ser Leu Ala Pro Pro Glu Val Asp Phe Asp Arg Leu Leu Ala Ser
        115                 120                 125


Leu Gln Asp Leu Ser Glu Leu Val Val Glu Gly Asp Thr Gln Val Thr
    130                 135                 140


Pro Val Pro Gly Gly Ala Arg Leu Arg Thr Leu Glu Pro Ile Pro Leu
145.                150                 155                 160


Lys Leu Tyr Arg Asn Gly Ile Met Met Phe Asp Gly Pro Phe Gln Pro
                165                 170                 175


Phe Tyr Asp Pro Ser Thr Gln Arg Cys Leu Arg Asp Ile Leu Asp Gly
            180                 185                 190
```

```
Phe Phe Pro Ser Glu Leu Gln Arg Leu Tyr Pro Asn Gly Val Pro Phe
        195                 200                 205


Lys Val Ser Asp Leu Arg Asn Gln Val Tyr Leu Glu Asp Gly Leu Asp
    210                 215                 220


Pro Phe Pro Gly Glu Gly Arg Val Val Gly Arg Gln Arg Met His Lys
225                 230                 235                 240


Ala Leu Asp Arg Val Glu Glu His Pro Gly Ser Arg Met Thr Ala Glu
                245                 250                 255


Lys Phe Leu Asn Arg Leu Pro Lys Phe Val Ile Arg Gln Gly Glu Val
            260                 265                 270


Ile Asp Ile Arg Gly Pro Ile Arg Asp Thr Leu Gln Asn Cys Cys Pro
        275                 280                 285


Leu Pro Ala Arg Ile Gln Glu Ile Val Val Glu Thr Pro Thr Leu Ala
    290                 295                 300


Ala Glu Arg Glu Arg Ser Gln Glu Ser Pro Asn Thr Pro Ala Pro Pro
305                 310                 315                 320


Leu Ser Met Leu Arg Ile Lys Ser Glu Asn Gly Glu Gln Ala Phe Leu
            325                 330                 335


Leu Met Met Gln Pro Asp Asn Thr Ile Gly Asp Val Arg Ala Leu Leu
            340                 345                 350


Ala Gln Ala Arg Val Met Asp Ala Ser Ala Phe Glu Ile Phe Ser Thr
        355                 360                 365


Phe Pro Pro Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala
    370                 375                 380


Gly Leu Val Pro Lys Ala Ala Leu Leu Leu Arg Ala Arg Arg Ala Pro
385                 390                 395                 400


Lys Ser Ser Leu Lys Phe Ser Pro Gly Pro Cys Pro Gly Pro Gly Pro
            405                 410                 415


Gly Pro Ser Pro Gly Pro Gly Pro Gly Ser Ser Pro Cys Pro Gly Pro
            420                 425                 430


Ser Pro Ser Pro Gln
        435
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<210> 3
<211> 60
<212> DNA
<213> Homo sapiens

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ttcagcacat tcccgcccac cctctaccag gacgatacac tcacgctgca ggctgcaggc        60


<210>  4
<211>  20
<212>  PRT
<213>  Homo sapiens

<400>  4

Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu
1                5                10                  15


Gln Ala Ala Gly
            20


<210>  5
<211>  42
<212>  DNA
<213>  Homo sapiens

<400>  5
accctctacc aggacgatac actcacgctg caggctgcag gc                          42


<210>  6
<211>  14
<212>  PRT
<213>  Homo sapiens

<400>  6

Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly
1                5                10


<210>  7
<211>  1028
<212>  DNA
<213>  Homo sapiens

<400>  7
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aagacagtct cagagcatgg cgagagggac tggatgacag ccaagaagtt ctggaagcca       120

ggggactcat tggcgccccc tgaggtggac tttgacaggc tgctggccag cctgcaggat       180

cttagtgagc tggtggtaga gggtgacacc caagtgacac cagtgcccgg cggggcacgg       240

ctgcgtaccc tcgagcccat cccgctgaag ctctaccgga atggcatcat gatgttcgac       300

gggcccttcc agcccttcta cgatccctcc acacagcgct gcctccgaga catattggat       360

ggcttctttc cctcagagct ccagcgactg taccccaatg gggtcccctt taaggtgagt       420

gacttgcgca atcaggtcta cctggaggat ggactggacc ccttcccagg cgagggccgt       480

gtggtgggca ggcagcggat gcacaaggcc ttggacaggg tggaggagca cccaggctcc       540

aggatgactg ctgagaaatt tctgaacagg ctccccaagt tttgatccgg caaggcgagg       600

tgattgacat ccggggcccc atcagggaca ccttgcagaa ctgctgccca ttgcctgccc      .660
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agtcacccaa cacaccggca ccccgctct ccatgctgcg catcaagtct gagaatgggg   780

aacaggcctt cctactgatg atgcagcctg acaacaccat tggggacgtg cgagctctgc   840

tagcgcaggc cagggtcatg gatgcctctg cctttgagat cttcagcaca ttcccgccca   900

ccctctacca ggacgataca ctcacgctgc aggctgcagg ccttgtgccc aaagcagcac   960

tgctgctgcg ggcacgccga gccccgaagt ccagcctgaa attcagtcct ggtccctgtc   1020

ccggtccc   1028

<210>   8
<211>   343
<212>   PRT
<213>   Homo sapiens

<400>   8

Leu Ser Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp Gln Glu
1   5   10   15

Asp Ser Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp Trp Met
            20   25   30

Thr Ala Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro Pro Glu
        35   40   45

Val Asp Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser Glu Leu
    50   55   60

Val Val Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly Ala Arg
65   70   75   80

Leu Arg Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn Gly Ile
                85   90   95

Met Met Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser Thr Gln
            100   105   110

Arg Cys Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu Leu Gln
        115   120   125

Arg Leu Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu Arg Asn
    130   135   140

Gln Val Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu Gly Arg
145   150   155   160

Val Val Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val Glu Glu
                165   170   175

His Pro Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg Leu Pro
            180   185   190

```
Lys Phe Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly Pro Ile
        195             200         205

Arg Asp Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile Gln Glu
    210             215             220

Ile Val Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg Ser Gln
225             230             235             240

Glu Ser Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg Ile Lys
            245             250             255

Ser Glu Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro Asp Asn
            260             265             270

Thr Ile Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp
        275             280             285

Ala Ser Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln
    290             295             300

Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala
305             310             315             320

Leu Leu Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys Phe Ser
            325             330             335

Pro Gly Pro Cys Pro Gly Pro
            340
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```
<210>  9
<211>  6
<212>  PRT
<213>  Homo sapiens

<400>  9

Phe Ser Thr Phe Pro Pro
1                   5


<210>  10
<211>  6
<212>  PRT
<213>  Homo sapiens

<400>  10

Leu Val Pro Lys Ala Ala
1                   5


<210>  11
<211>  294
<212>  DNA
<213>  Homo sapiens
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<400> 11
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cttgtgccca aagcagcact gctgctgcgg gcacgccgag ccccgaagtc cagcctgaaa   ·180

ttcagtcctg gtccctgtcc cggtcccggt cccggcccca gtcccggtcc cggtcccggc   240

tccagtccct gtcccggacc cagtcccagc ccccaataaa gcacccaccc cctc   294

<210> 12
<211> 92
<212> PRT
<213> Homo sapiens

<400> 12

Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp Ala Ser
1   5   10   15

Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp
            20   25   30

Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala Leu Leu
        35   40   45

Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys Phe Ser Pro Gly
    50   55   60

Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly Pro Gly Pro Gly
65   70   75   80

Ser Ser Pro Cys Pro Gly Pro Ser Pro Ser Pro Gln
                85   90

<210> 13
<211> 19
<212> DNA
<213> ARTIFICIAL

<220>
<223> PCR primer sequence

<400> 13
tccagcatgg tgtgtctga   19

<210> 14
<211> 18
<212> DNA
<213> artificial

<220>
<223> PCR primer sequence

<400> 14
ccttgaatgt ggtcatct   18

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<210>  15
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<212>  DNA
<213>  artificial

<220>
<223>  PCR primer sequence

<400>  15
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<210>  16
<211>  20
<212>  DNA
<213>  artificial

<220>
<223>  PCR primer sequence

<400>  16
ccaccgcggc ccgctcgtct                                                   20


<210>  17
<211>  20
<212>  PRT
<213>  Homo sapiens

<400>  17

Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu
1               5                   10                  15


Gln Ala Ala Gly
            20


<210>  18
<211>  20
<212>  PRT
<213>  Homo sapiens

<400>  18

Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val
1               5                   10                  15


Pro Lys Ala Ala
            20


<210>  19
<211>  1771
<212>  DNA
<213>  Homo sapiens

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tttcccaagc accaccaggc caaaggtctc tcagttcaga gcagaaagcc gtatacccag    120

aggagcaggc agataacaga aacttccaga aacctctgtg gagacagtgg aagaggcaaa    180

agggagttcc tgacagctgg attctagaag tagaactatg agctcacctt tggcctccct    240
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9

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tagcaagacc cgaaaagtgc ccctgccctc ggagcctatg aatcctggga ggcgaggaat    300

ccgcatctat ggagatgaag atgaggtgga catgttgagt gatgggtgtg gctcggaaga    360

aaagatctca gtcccttcct gctatggcgg cataggtgcc cctgtgagtc ggcaagtccc    420

tgcatcccat gactcggagc tgatggcctt catgacgagg aagttgtggg acctggagca    480

gcaggtgaag gcccagactg atgagatact gtccaaggat cagaagatag cggccctaga    540

ggacctggtg cagaccctcc ggccacaccc agccgaggca accctgcagc ggcaggagga    600

actggagacg atgtgtgtgc agctgcagcg gcaggtcagg gagatggagc ggttcctcag    660

tgactatggc ctgcagtggg tgggcgagcc catggaccag gaggactcag agagcaagac    720

agtctcagag catggcgaga gggactggat gacagccaag aagttctgga agccagggga    780

ctcattggcg cccccctgagg tggactttga caggctgctg gccagcctgc aggatcttag    840

tgagctggtg gtagagggtg acacccaagt gacaccagtg cccggcgggg cacggctgcg    900

taccctcgag cccatcccgc tgaagctcta ccggaatggc atcatgatgt cgacgggcc     960

cttccagccc ttctacgatc cctccacaca gcgctgcctc cgagacatat tggatggctt    1020

cttttccctca gagctccagc gactgtaccc caatgggggtc ccctttaagg tgagtgactt    1080

gcgcaatcag gtctacctgg aggatggact ggaccccttc ccaggcgagg gccgtgtggt    1140

gggcaggcag cggatgcaca aggccttgga cagggtggag gagcacccag gctccaggat    1200

gactgctgag aaatttctga acaggctccc caagtttgtg atccggcaag gcgaggtgat    1260

tgcatccgg ggcccca tca gggacacctt gcagaactgc tgcccattgc ctgcccggat    1320

ccaggagatt gtggtggaga cgcccacctt ggccgctgag cgagagagga gccaggagtc    1380

acccaacaca ccggcacccc cgctctccat gctgcgcatc aagtctgaga atggggaaca    1440

ggccttccta ctgatgatgc agcctgacaa caccattggg gacgtgcgag ctctgctagc    1500

gcaggccagg gtcatggatg cctctgcctt tgagatcttc agcacattcc cgcccaccct    1560

ctaccaggac gatacactca cgctgcaggc tgcaggcctt gtgcccaaag cagcactgct    1620

gctgcgggca cgccgagccc cgaagtccag cctgaaattc agtcctggtc cctgtcccgg    1680

tcccggtccc ggccccagtc ccggtcccgg tcccggctcc agtccctgtc ccggacccag    1740

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```
<210>  20
<211>  512
<212>  PRT
<213>  Homo sapiens

<400>  20

Met Ser Ser Pro Leu Ala Ser Leu Ser Lys Thr Arg Lys Val Pro Leu
1               5                   10                  15


Pro Ser Glu Pro Met Asn Pro Gly Arg Arg Gly Ile Arg Ile Tyr Gly
                20                  25                  30
```

```
Asp Glu Asp Glu Val Asp Met Leu Ser Asp Gly Cys Gly Ser Glu Glu
        35              40                  45

Lys Ile Ser Val Pro Ser Cys Tyr Gly Gly Ile Gly Ala Pro Val Ser
        50              55                  60

Arg Gln Val Pro Ala Ser His Asp Ser Glu Leu Met Ala Phe Met Thr
65                  70              75                  80

Arg Lys Leu Trp Asp Leu Glu Gln Gln Val Lys Ala Gln Thr Asp Glu
                85              90                  95

Ile Leu Ser Lys Asp Gln Lys Ile Ala Ala Leu Glu Asp Leu Val Gln
            100             105             110

Thr Leu Arg Pro His Pro Ala Glu Ala Thr Leu Gln Arg Gln Glu Glu
        115             120             125

Leu Glu Thr Met Cys Val Gln Leu Gln Arg Gln Val Arg Glu Met Glu
        130             135             140

Arg Phe Leu Ser Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp
145             150             155             160

Gln Glu Asp Ser Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp
            165             170                 175

Trp Met Thr Ala Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro
        180             185             190

Pro Glu Val Asp Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser
        195             200             205

Glu Leu Val Val Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly
    210             215             220

Ala Arg Leu Arg Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn
225             230             235             240

Gly Ile Met Met Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser
            245             250             255

Thr Gln Arg Cys Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu
        260             265             270

Leu Gln Arg Leu Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu
        275             280             285

Arg Asn Gln Val Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu
    290             295             300
```

11

```
Gly Arg Val Val Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val
305               310             315             320


Glu Glu His Pro Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg
              325             330             335


Leu Pro Lys Phe Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly
          340             345             350


Pro Ile Arg Asp Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile
          355             360             365


Gln Glu Ile Val Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg
      370             375             380


Ser Gln Glu Ser Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg
385             390             395             400


Ile Lys Ser Glu Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro
              405             410             415


Asp Asn Thr Ile Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val
          420             425             430


Met Asp Ala Ser Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu
          435             440             445


Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys
    450             455             460


Ala Ala Leu Leu Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys
465             470             475             480


Phe Ser Pro Gly Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly
              485             490             495


Pro Gly Pro Gly Ser Ser Pro Cys Pro Gly Pro Ser Pro Ser Pro Gln
          500             505             510
```

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